PEM's
Complete web table # 25 (PEM3) + # 47 (PEM6) are G1, rest are G3

Table 1. Previously characterized and novel Pan Endothelial Markers. The most abundant tags derived by summing the tags from Normal EC (N-EC's) and Tumor EC (T-EC's) SAGE libraries are listed in descending order. N-EC and T-EC SAGE libraries contained 96,694 and 96,588 SAGE tags respectively. For comparison, the corresponding number of SAGE tags found in cultured human umbilical vein endothelial cells (HUVEC), human dermal microvascular endothelial cells (HMVEC), and non-endothelial cell lines (Cell Lines) are shown. The HUVEC SAGE library contained 290,000 tags and the HMVEC library 111,000 tags. Non-endothelial cell lines consisted of 1.8×10^6 tags derived from a total of 14 different cancer cell lines including colon, breast, lung, and pancreatic cancers, as well as one non-transformed keratinocyte cell line, two kidney epithelial cell lines, and normal monocytes. Tag numbers for each group were normalized to 100,000 transcripts. A 'Description' of the gene product corresponding to each tag is given, followed by alternative names in parenthesis. The sequence CATG precedes all tags and the 15th base (11th shown) was determined as previously described by Velculescu et. al. (Nat Genet 1999 Dec;23(4):387-8).

no.	Tag Sequence	N-EC's	T-EC's	HUVEC	HMVEC	Cell Lines	Description
1	CATATCATTAA	247	501	130	87	2	angiomodulin (ANG, IGFBP-7, IGFBP-rP1, Mac25, TAF)
2	TGCACTTCAAG	328	141	0	0	0	hevin
3	TTTGCACCTTT	165	84	191	115	4	connective tissue growth factor (CTGF, IGFBP-rP2)
4	CCCTTGTCCG	131	104	1	1	0	ESTs
5	TTGCTGACTTT	73	131	2	14	1	collagen, type VI, alpha 1
6	ACCATTGGATT	102	67	0	0	2	interferon induced transmembrane protein 1 (9-27, Leu 13)
7	ACACTTCTTTC	104	44	60	62	2	guanine nucleotide binding protein 11
8	TTCTGCTCTTG	71	67	118	72	0	von Willebrand factor
9	TCCCTGGCAGA	66	68	3	13	3	cysteine-rich protein 2 (CRP-2, ESP-1, SmLIM)
10	TAATCCTCAAG	26	106	34	16	1	collagen, type XVIII, alpha 1
11	ATGTCTTTTCT	58	65	17	17	3	insulin-like growth factor-binding protein 4
12	GGGATTAAAGC	40	67	30	14	2	CD146 (S-Endo 1, P1H12, Muc18, MCAM, Mel-CAM)
13	TTAGTGTCGTA	38	69	9	13	0	SPARC (osteonectin, BM-40)
14	TTCTCCCAAAT	20	86	16	64	2	collagen, type IV, alpha 2
15	GTGCTAAGCGG	24	74	0	10	2	collagen, type VI, alpha 2
16	GTTTATGGATA	35	56	11	11	1	matrix Gla protein (MGP)
17	CCCTTTCACAC	52	33	0	0	0	ESTs, Weakly similar to HPBRII-7 protein
18	TGTTCTGGAGA	58	27	18	56	2	gap junction protein, alpha 1, 43kD (connexin 43)
19	AAGATCAAGAT	34	50	2	4	1	actin, alpha 1, skeletal muscle / actin, alpha 2, smooth muscle, aorta
20	TCTCTGAGCAT	32	48	0	0	0	aggrecanase 1 (metalloproteinase with thrombospondin type 1 motifs, 4)
21	CAGGTTTCATA	22	56	0	0	0	small inducible cytokine subfamily B (Cys-X-Cys), member 14 (BRAK)
22	GCACAAGTTCT	43	25	6	22	0	calcitonin receptor-like receptor activity modifying protein 2
23	AGCTTGTGGCC	45	23	0	0	0	calcitonin receptor-like receptor activity modifying protein 3
24	CTTCTGGATAA	13	54	12	0	0	cell division cycle 42 (GTP-binding protein, 25kD)
G1 25	CAACAATAATA	42	25	13	6	0	ESTs

	26 ACCGGCGCCCG	50	15	0	0	0	tetranectin (plasminogen-binding protein)
	27 GGAAGCTAAGT	35	27	0	5	1	osteoblast specific factor 2 (fasciclin I-like)
	28 GCAATTTAACC	38	21	0	3	0	solute carrier family 21 (prostaglandin transporter), member 2
	29 GATAACTACAT	18	35	4	4	0	angiomodulin (ANG, IGFBP-7, IGFBP-rP1, Mac25, TAF)
	30 TATGAGGGTAA	19	30	40	2	0	regulator of G-protein signalling 5
	31 CCACGGGATTC	10	39	0	0	0	collagen, type III, alpha 1
	32 TTTACAAAGAG	26	21	0	1	1	carboxypeptidase E
	33 CCCAGTAAGAT	22	25	0	16	1	cysteine and glycine-rich protein 2 (LIM domain only, smooth muscle)
	34 ACAAAGCATTT	26	20	0	14	1	Human insulin-like growth factor binding protein 5 (IGFBP5) mRNA
	35 GCCTGTCCCTC	8	38	22	11	0	ESTs / biglycan
	36 TACTTTATAAG	25	21	1	1	0	metalloproteinase with thrombospondin type 1 motifs (ADAMTS1, METH-1)
	37 TGTTTAATACA	15	29	2	1	1	ESTs / erythrocyte membrane protein band 4.1-like 2
	38 GTCCCTGCCTT	18	25	1	1	0	glutathione S-transferase M2 (muscle)
	39 GAGCCATCATA	21	21	2	2	1	ESTs / GTP-binding protein overexpressed in skeletal muscle
	40 GGCCCTACAGT	26	13	2	3	0	ESTs / KIAA0821 protein
	41 GCTAACCCCTG	7	31	0	1	0	ESTs
	42 ATCACACAGCT	19	18	0	0	0	thyroid and eye muscle autoantigen D1 (64kD)
	43 ACAAGTACTGT	18	19	36	27	0	cadherin 5, VE-cadherin (vascular epithelium)
	44 TCACCGTGGAC	20	17	0	1	0	selectin P (granule membrane protein 140kD, antigen CD62)
	45 ACATTCCAAGT	18	18	0	1	1	tissue inhibitor of metalloproteinase 3
	46 GAGCCTGGATA	6	29	0	0	0	chondroitin sulfate proteoglycan 4 (melanoma-associated)
G1	47 GGCACTCCTGT	22	13	19	12	0	ESTs
	48 TCACAGCCCCC	20	15	8	5	0	ESTs
	49 TGCCAGGTGCA	10	23	0	1	0	albumin
	50 TGGGAAACCTG	11	22	0	1	1	eukaryotic translation initiation factor 4 gamma, 1
	51 TTTCATCCACT	20	13	0	2	0	ESTs, KIAA0362 protein
	52 AACAGGGGCCA	15	18	0	0	1	interferon, alpha-inducible protein (clone IFI-6-16)
	53 ACTGAAAGAAG	6	26	0	0	1	complement component 1, s subcomponent
	54 ACCGTTCTGTA	8	24	10	6	0	transcription factor 4
	55 ATACTATAATT	25	6	2	0	0	ESTs
	56 TTTGTATAGAA	17	15	4	5	1	hect domain and RLD 2
	57 GTAATGACAGA	20	11	1	1	1	stanniocalcin
	58 AATAGGGGAAA	13	19	4	1	0	ESTs, KIAA1075 protein
	59 GTGCTACTTCT	5	25	2	18	0	collagen, type IV, alpha 1
	60 CCGGCCCCTCC	6	24	0	0	1	peanut (Drosophila)-like 2
	61 TTGAATTTGTT	19	10	1	1	0	RNA-binding protein gene with multiple splicing
	62 CGAGAGTGTGA	22	6	0	0	0	ESTs
	63 CCCTGTTCAGC	14	15	38	24	0	tyrosine kinase with IgG and EGF homology domains (Tie)

64	CAGATGGAGGC	18	10	1	9	0	ESTs
65	AGGCTCCTGGC	8	20	0	0	0	ESTs
66	TCTGCTTCTAG	20	8	40	15	0	ESTs
67	GGCTTAGGATG	18	9	10	14	0	ESTs
68	GGTTGTTGCGG	6	21	0	0	1	ESTs
69	ACAAGTACCCA	5	22	4	5	0	P311 protein
70	CTTCTCTTGAG	18	9	1	4	1	basic transcription element binding protein 1
71	GCTAATAATGT	10	17	0	2	0	KIAA1077 protein
72	TGTGCTTTTTT	10	15	1	4	0	KIAA0758 protein / protein kinase, cAMP-dependent, catalytic, alpha
73	CATCACGGATC	17	8	0	1	0	interleukin 1 receptor, type I
74	GCAGCAGCAGC	6	18	0	2	0	T-box 2
75	TGACTGTATTA	13	11	0	0	0	ESTs / amine oxidase, copper containing 3 (vascular adhesion protein 1)
76	GAATGCTCTTG	6	18	0	11	0	gap junction protein, alpha 4, 37kD (connexin 37)
77	GTAGTTCTGGA	18	6	0	5	0	ESTs, clone 23698 mRNA
78	TCCCCTCTCTC	6	17	0	0	0	periodontal ligament fibroblast protein
79	GGGCAGTGGCT	5	18	12	5	0	ESTs, DKFZP586B0621 protein
80	AAATATGTGTT	19	4	13	3	0	ESTs
81	GTCATTTTCTA	11	11	10	2	0	transcription factor 8 (represses interleukin 2 expression)
82	CTCTCCAAACC	14	8	0	0	0	complement component 1 inhibitor (angioedema, hereditary)
83	TTAATGTGTAA	4	18	0	0	0	guanylate cyclase 1, soluble, beta 3
84	TCAAGCAATCA	13	9	0	1	0	ESTs
85	GAAGACACTTG	15	7	1	0	0	ESTs
86	GGGTAGGGTGA	6	15	0	0	1	integrin, alpha 7
87	TGGAACAGTGA	10	10	10	5	0	ESTs
88	GAGTGGCTACC	10	9	0	0	0	ESTs
89	GTCAGGGTCCC	13	7	0	9	0	decidual protein induced by progesterone
90	GTCAGTCACTT	14	6	4	1	0	hairy (Drosophila)-homolog
91	AGCAGAGACAA	14	6	1	10	0	natriuretic peptide receptor A - guanylate cyclase A
92	AGCGATGGAGA	9	10	0	0	0	ESTs
93	CGTGGGGTGTA	9	10	17	3	0	

TEM's complete web table

Table 2. SAGE tags elevated in tumor endothelium. The top 46 tags with the highest tumor EC (T-EC's) to normal EC (N-EC's) tag ratios are listed in descending order. To calculate tag ratios, a value of 0.5 was assigned in cases where zero tags were observed. The SAGE libraries are the same as those listed in Table 1. Tag numbers for each group were normalized to 100,000 transcripts. A 'Description' of the gene product corresponding to each tag is given, followed by alternative names in parenthesis. †; multiple tags for this gene are due to alternative polyadenylation sites.

no.	Tag Sequence	N-EC's	T-EC's	HUVEC	HMVEC	Cell Lines	Description
1	GGGGCTGCCCA	0	28	0	2	0	ESTs, similarity to thrombomodulin TEM1
2	GATCTCCGTGT	0	25	0	0	0	ESTs, similarity to rat Rhes ras-related protein TEM2
3	CATTTTTATCT	0	23	0	0	0	ESTs
4	CTTTCTTTGAG	0	22	6	20	1	regulated in glioma-like 7-1 (Dkk-3/ REIC)
5	TATTAACTCTC	0	21	1	3	1	ESTs, similarity to JNK interacting protein-3a
6	CAGGAGACCCC	0	16	2	0	0	MMP-11 (stromelysin 3)
7	GGAAATGTCAA	1	31	53	22	1	MMP-2 (gelatinase A, 72kD type IV collagenase)
8	CCTGGTTCAGT	0	15	0	0	0	ESTs
9	TTTTTAAGAAC	0	14	1	4	0	ESTs
10	TTTGGTTTTCC	5	139	0	16	0	collagen, type I, alpha 2, transcript A†
11	ATTTTGTATGA	0	13	4	8	0	nidogen (entactin)
12	ACTTTAGATGG	1	23	0	15	0	collagen, type VI, alpha 3
13	GAGTGAGACCC	3	63	0	0	1	Thy-1 cell surface antigen
14	GTACACACACC	0	10	0	0	0	ESTs / cystatin S
15	CCACAGGGGAT	2	38	0	2	1	collagen, type III, alpha 1
16	TTAAAAGTCAC	1	19	1	3	1	ESTs
17	ACAGACTGTTA	4	74	0	0	0	ESTs, similarity with sea squirt nidogen TEM7
18	CCACTGCAACC	1	18	0	1	0	
19	CTATAGGAGAC	1	18	1	1	0	ESTs, similarity with homeobox protein DLX-3 TEM8
20	GTTCCACAGAA	0	9	0	3	0	collagen, type I, alpha 2, transcript B†
21	TACCACCTCCC	0	9	4	1	1	ESTs / pregnancy specific beta-1-glycoprotein 1
22	GCCCTTTCTCT	1	17	3	1	2	endo180 lectin
23	TTAAATAGCAC	2	33	0	4	0	collagen, type I, alpha 1
24	AGACATACTGA	1	16	1	0	0	ESTs, DKFZP434G162 protein
25	TCCCCCAGGAG	1	16	0	0	0	bone morphogenetic protein 1 (metalloprotease)
26	AGCCCAAAGTG	0	8	0	0	0	
27	ACTACCATAAC	0	8	0	0	0	slit (Drosophila) homolog 3 (MEGF5)
28	TACAAATCGTT	0	8	0	0	0	KIAA0672 gene product

see table 2 from paper for G1, G2 or G3

all G3

29	TTGGGTGAAAA	0	8	0	0	0	ESTs
30	CATTATCCAAA	0	8	0	0	0	integrin, alpha 1
31	AGAAACCACGG	0	8	2	7	0	collagen, type IV, alpha 1
32	ACCAAAACCAC	0	8	0	3	0	
33	TGAAATAAAC	0	8	3	1	1	
34	TTTGGTTTCC	1	15	0	0	0	ESTs
35	GTGGAGACGGA	1	15	1	2	1	ESTs
36	TTTGTGTTGTA	1	14	2	0	0	collagen, typeXII, alpha 1
37	TTATGTTTAAT	3	39	0	0	1	lumican
38	TGGAAATGACC	15	179	0	40	0	ESTs / collagen, type I, alpha 1
39	TGCCACACAGT	1	13	0	2	0	transforming growth factor, beta 3
40	GATGAGGAGAC	3	35	0	18	1	collagen, type I, alpha 2, transcript C†
41	ATCAAAGGTTT	2	23	0	0	0	ESTs, DKFZp564O222 mRNA
42	AGTCACATAGT	1	11	2	0	0	cell division cycle 42 (GTP-binding protein)
43	TTCGGTTGGTC	4	45	0	19	0	
44	CCCCACACGGG	2	21	0	0	0	ESTs
45	GGCTTGCCTTT	1	10	0	10	1	
46	ATCCCTTCCCG	1	10	1	0	0	peanut-like protein 1

Table 3. Detection of transcripts in various tumor types by RT-PCR and in situ hybridization (ISH). The "+" sign indicates the presence of a robust RT-PCR product or stong positive staining of vessels by in situ hybridization. The "-" sign indicates an undetectable signal by in situ hybridization or an absent or barely detectable transcript by RT-PCR. The "+/-" sign indicates a very weak signal in a limited number vessels by in situ hybridization.

		TEM1	TEM3	TEM4	TEM5	TEM7	TEM8	TEM9	vWF	Hevin
RT-PCR	Colon Nor.	-	-	-	-	-	-	-	+	ND
	Colon Tum.	+	+	+	+	+	+	+	+	ND
ISH	Colon Nor.	-	-	-	-	-	-	-	+	+
	Colon Tum.	+	+	+	+	+	+	+	+	+
	Liver Met.	+	+/-	+	+	+	+	+	+/-	ND
	Lung Tum.	+	ND	+	+	+	+	+	+	+
	Brain Tum.	+	ND	ND	ND	+	ND	ND	+	+*
	Corpus Lut.	+	+	+	+	+	-	+	+	+
	Wound	+	ND	+	ND	+/-	+/-	ND	+	+

* hevin was localized to both endothelial cells and malignant cells in brain tissue.
ND: not determined.

www.sagenet.org\angio\table3.htm (to be posted upon publication)

Table 4. SAGE tags elevated in normal endothelium. The top 46 tags with the highest normal EC (N-EC's) to tumor EC (T-EC's) tag ratios are listed in descending order. To calculate tag ratios, a value of 0.5 was assigned in cases where zero tags were observed. The SAGE libraries are the same as those listed in Table 1. Tag numbers for each group were normalized to 100,000 transcripts. A 'Description' of the gene product corresponding to each tag is given, followed by alternative names in parenthesis.

no.	Tag Sequence	N-EC's	T-EC's	HUVEC	HMVEC	Cell Lines	Description
1	TCTCACGTCT	26	0	0	0	0	mucosal vascular addressin cell adhesion molecule 1
2	CTAGCGTTTT	19	0	4	14	0	serum deprivation response (phosphatidylserine-binding protein)
3	GTGGCTGACG	18	0	1	0	0	ESTs / intercellular adhesion molecule 4
4	CTCTTAAAAA	34	1	1	0	0	small inducible cytokine subfamily A (Cys-Cys), member 14
5	TGGGAAGAGG	16	0	3	4	1	ESTs
6	GTTTAAGGAT	16	0	0	0	0	ESTs
7	CTTTGTTTTG	15	0	56	32	1	endothelin 1 / ribosomal protein L27
8	ATTGCCAATC	14	0	0	4	0	TU3A protein
9	TGTTGAAAAA	21	1	1	0	0	selectin E (endothelial adhesion molecule 1)
10	ACAAAAAGGC	21	1	0	6	0	TU3A protein
11	AAGATGCACAC	21	1	1	1	1	phosphodiesterase I - nucleotide pyrophosphatase 2 (autotaxin)
12	GTAGAGGAAA	10	0	0	9	0	platelet/endothelial cell adhesion molecule (CD31 antigen)
13	TTGTTCAAGG	10	0	0	1	0	ESTs
14	CTCTTCAAAAA	19	1	1	0	0	ESTs / small inducible cytokine subfamily A, member 14
15	TATTAAAATA	18	1	6	9	1	transforming growth factor, beta receptor II (70-80kD)
16	GAATTCACCA	9	0	1	14	0	ESTs
17	AAGGAGAACT	9	0	0	0	0	small inducible cytokine subfamily A, member 14
18	AATATCTGAC	9	0	2	2	2	active BCR-related gene
19	TCAGTGACCAG	17	1	4	7	2	protein kinase C eta
20	GCAAAGTGCC	32	2	1	5	0	ESTs
21	TAAATACTTG	8	0	2	0	0	ESTs (2 unigene clusters)
22	GTCACTAATT	8	0	1	0	0	ESTs
23	ATAACCTGCA	8	0	0	0	0	signaling lymphocytic activation molecule
24	TGCATCTGTGC	46	3	1	1	0	ESTs / glycogenin 2
25	TAAAGGCACA	15	1	4	3	0	LIM binding domain 2
26	GACCGCGGCT	73	5	11	7	0	claudin 5
27	ACTCCGGTGT	14	1	0	8	0	ESTs

28	CTTCTCACCT	27	2	3	1	0	GTP-binding protein
29	TCGTGCTTTG	13	1	0	0	0	ESTs
30	GAGCAGTGCT	13	1	4	2	1	feline sarcoma viral (v-fes) - Fujinami avian sarcoma viral (v-fps) homolog
31	CTCTAAAAAA	10	1	0	1	0	ESTs
32	GAAACCCGGT	10	1	0	0	1	phospholipase C, beta 4
33	AACACAGTGC	10	1	7	15	1	ESTs

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There are 76 pages of specification. From page No 77 – 305 are sequence listing

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